## SEQUENCE LISTING

<110> ABBOTT, Catherine Anne
       GORRELL, Mark Douglas

<120> DIPEPTIDYL PEPTIDASES

<130> GH-007

<150> PCT/AU00/01085
<151> 2000-09-11

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<150> AU PQ2762
<151> 1999-09-10

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<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 882
<212> PRT
<213> Homo Sapiens

<400> 1

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Glu Pro Phe Tyr Val Glu Arg Tyr Ser Trp Ser Gln Leu Lys Lys Leu
            35                  40                  45
Leu Ala Asp Thr Arg Lys Tyr His Gly Tyr Met Met Ala Lys Ala Pro
    50                  55                  60
His Asp Phe Met Phe Val Lys Arg Asn Asp Pro Asp Gly Pro His Ser
65                  70                  75                  80
Asp Arg Ile Tyr Tyr Leu Ala Met Ser Gly Glu Asn Arg Glu Asn Thr
                85                  90                  95
Leu Phe Tyr Ser Glu Ile Pro Lys Thr Ile Asn Arg Ala Ala Val Leu
                100                 105                 110
Met Leu Ser Trp Lys Pro Leu Leu Asp Leu Phe Glu Ala Thr Leu Asp
                115                 120                 125
Tyr Gly Met Tyr Ser Arg Glu Glu Glu Leu Leu Arg Glu Arg Lys Arg
            130                 135                 140
Ile Gly Thr Val Gly Ile Ala Ser Tyr Asp Tyr His Gln Gly Ser Gly
145                 150                 155                 160
Thr Phe Leu Phe Gln Ala Gly Ser Gly Ile Tyr His Val Lys Asp Gly
                165                 170                 175
Gly Pro Gln Gly Phe Thr Gln Gln Pro Leu Arg Pro Asn Leu Val Glu
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              180                   185                   190
Thr Ser Cys Pro Asn Ile Arg Met Asp Pro Lys Leu Cys Pro Ala Asp
              195                   200                   205
Pro Asp Trp Ile Ala Phe Ile His Ser Asn Asp Ile Trp Ile Ser Asn
              210                   215                   220
Ile Val Thr Arg Glu Glu Arg Arg Leu Thr Tyr Val His Asn Glu Leu
225                   230                   235                   240
Ala Asn Met Glu Glu Asp Ala Arg Ser Ala Gly Val Ala Thr Phe Val
              245                   250                   255
Leu Gln Glu Glu Phe Asp Arg Tyr Ser Gly Tyr Trp Trp Cys Pro Lys
              260                   265                   270
Ala Glu Thr Thr Pro Ser Gly Gly Lys Ile Leu Arg Ile Leu Tyr Glu
              275                   280                   285
Glu Asn Asp Glu Ser Glu Val Glu Ile Ile His Val Thr Ser Pro Met
              290                   295                   300
Leu Glu Thr Arg Arg Ala Asp Ser Phe Arg Tyr Pro Lys Thr Gly Thr
305                   310                   315                   320
Ala Asn Pro Lys Val Thr Phe Lys Met Ser Glu Ile Met Ile Asp Ala
              325                   330                   335
Glu Gly Arg Ile Ile Asp Val Ile Asp Lys Glu Leu Ile Gln Pro Phe
              340                   345                   350
Glu Ile Leu Phe Glu Gly Val Glu Tyr Ile Ala Arg Ala Gly Trp Thr
              355                   360                   365
Pro Glu Gly Lys Tyr Ala Trp Ser Ile Leu Leu Asp Arg Ser Gln Thr
              370                   375                   380
Arg Leu Gln Ile Val Leu Ile Ser Pro Glu Leu Phe Ile Pro Val Glu
385                   390                   395                   400
Asp Asp Val Met Glu Arg Gln Arg Leu Ile Glu Ser Val Pro Asp Ser
              405                   410                   415
Val Thr Pro Leu Ile Ile Tyr Glu Glu Thr Thr Asp Ile Trp Ile Asn
              420                   425                   430
Ile His Asp Ile Phe His Val Phe Pro Gln Ser His Glu Glu Glu Ile
              435                   440                   445
Glu Phe Ile Phe Ala Ser Glu Cys Lys Thr Gly Phe Arg His Leu Tyr
              450                   455                   460
Lys Ile Thr Ser Ile Leu Lys Glu Ser Lys Tyr Lys Arg Ser Ser Gly
465                   470                   475                   480
Gly Leu Pro Ala Pro Ser Asp Phe Lys Cys Pro Ile Lys Glu Glu Ile
              485                   490                   495
Ala Ile Thr Ser Gly Glu Trp Glu Val Leu Gly Arg His Gly Ser Asn
              500                   505                   510
Ile Gln Val Asp Glu Val Arg Arg Leu Val Tyr Phe Glu Gly Thr Lys
              515                   520                   525
Asp Ser Pro Leu Glu His His Leu Tyr Val Val Ser Tyr Val Asn Pro
              530                   535                   540
Gly Val Val Ser Arg Leu Val Asp Arg Gly Tyr Ser His Ser Cys Cys
545                   550                   555                   560
Ile Ser Gln His Cys Asp Phe Phe Ile Ser Lys Tyr Ser Asn Gln Lys
              565                   570                   575
Asn Pro His Cys Val Ser Leu Tyr Lys Leu Ser Ser Pro Glu Asp Asp
              580                   585                   590
Pro Thr Cys Lys Thr Lys Glu Phe Trp Ala Thr Ile Leu Asp Ser Ala
              595                   600                   605
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Gly Pro Leu Pro Asp Tyr Thr Pro Pro Glu Ile Phe Ser Phe Glu Ser
    610                 615             620
Thr Thr Gly Phe Thr Leu Tyr Gly Met Leu Tyr Lys Pro His Asp Leu
625             630             635             640
Gln Pro Gly Lys Lys Tyr Pro Thr Val Leu Phe Ile Tyr Gly Gly Pro
            645             650             655
Gln Val Gln Leu Val Asn Asn Arg Phe Lys Gly Val Lys Tyr Phe Arg
            660             665             670
Leu Asn Thr Leu Ala Ser Leu Gly Tyr Val Val Val Ile Asp Asn
            675             680             685
Arg Gly Ser Cys His Arg Gly Leu Lys Phe Glu Gly Ala Phe Lys Tyr
    690             695             700
Lys Met Gly Gln Ile Glu Ile Asp Asp Gln Val Glu Gly Leu Gln Tyr
705             710             715             720
Leu Ala Ser Arg Tyr Asp Phe Ile Asp Leu Asp Arg Val Gly Ile His
            725             730             735
Gly Trp Ser Tyr Gly Gly Tyr Leu Ser Leu Met Ala Leu Met Gln Arg
            740             745             750
Ser Asp Ile Phe Arg Val Ala Ile Ala Gly Ala Pro Val Thr Leu Trp
    755             760             765
Ile Phe Tyr Asp Thr Gly Tyr Thr Glu Arg Tyr Met Gly His Pro Asp
    770             775             780
Gln Asn Glu Gln Gly Tyr Tyr Leu Gly Ser Val Ala Met Gln Ala Glu
785             790             795             800
Lys Phe Pro Ser Glu Pro Asn Arg Leu Leu Leu Leu His Gly Phe Leu
            805             810             815
Asp Glu Asn Val His Phe Ala His Thr Ser Ile Leu Leu Ser Phe Leu
            820             825             830
Val Arg Ala Gly Lys Pro Tyr Asp Leu Gln Ile Tyr Pro Gln Glu Arg
    835             840             845
His Ser Ile Arg Val Pro Glu Ser Gly Glu His Tyr Glu Leu His Leu
    850             855             860
Leu His Tyr Leu Gln Glu Asn Leu Gly Ser Arg Ile Ala Ala Leu Lys
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Val Ile
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<211> 3120
<212> DNA
<213> Homo Sapiens

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gagtggaggc ggcgcagcat gaagcggcgc aggcccgctc catagcgcac gtcgggacgg 180
tccgggcggg gccggggggа aggaaaatgc aacatggcag cagcaatgga aacagaacag 240
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cctaaattgg agcctttta tgttgagcgg tattcctgga gtcagcttaa aaagctgctt 360
gccgatacca gaaaatatca tggctacatg atggctaagg caccacatga tttcatgttt 420
gtgaagagga atgatccaga tggacctcat tcagacagaa tctattacct tgccatgtct 480
ggtgagaaca gagaaaatac actgttttat tctgaaattc ccaaaactat caatagagca 540
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gcagtcttaa tgctctcttg gaagcctctt ttggatcttt ttcaggcaac actggactat  600
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attgcttctt acgattatca ccaaggaagt ggaacatttc tgtttcaagc cggtagtgga  720
atttatcacg taaaagatgg agggccacaa ggatttacgc aacaaccttt aaggcccaat  780
ctagtggaaa ctagttgtcc caacatacgg atggatccaa aattatgccc cgctgatcca  840
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gaaaggagac tcacttatgt gcacaatgag ctagccaaca tggaagaaga tgccagatca  960
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<210> 3
<211> 310
<212> PRT
<213> Homo Sapiens

<400> 3
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 1               5                  10                  15
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Ser Tyr Val Asn Pro Gly Glu Val Thr Arg Leu Thr Asp Arg Gly Tyr
            20                  25                  30
Ser His Ser Cys Cys Ile Ser Gln His Cys Asp Phe Phe Ile Ser Lys
            35                  40                  45
Tyr Ser Asn Gln Lys Asn Pro His Cys Val Ser Leu Tyr Lys Leu Ser
            50                  55                  60
Ser Pro Glu Asp Asp Pro Thr Cys Lys Thr Lys Glu Phe Trp Ala Thr
65                  70                  75                  80
Ile Leu Asp Ser Ala Gly Pro Leu Pro Asp Tyr Thr Pro Pro Glu Ile
                85                  90                  95
Phe Ser Phe Glu Ser Thr Thr Gly Phe Thr Leu Tyr Gly Met Leu Tyr
            100                 105                 110
Lys Pro His Asp Leu Gln Pro Gly Lys Lys Tyr Pro Thr Val Leu Phe
            115                 120                 125
Ile Tyr Gly Gly Pro Gln Gly Gln Ile Glu Ile Asp Asp Gln Val Glu
            130                 135                 140
Gly Leu Gln Tyr Leu Ala Ser Arg Tyr Asp Phe Ile Asp Leu Asp Arg
145                 150                 155                 160
Val Gly Ile His Gly Trp Ser Tyr Gly Gly Tyr Leu Ser Leu Met Ala
                165                 170                 175
Leu Met Gln Arg Ser Asp Ile Phe Arg Val Ala Ile Ala Gly Ala Pro
            180                 185                 190
Val Thr Leu Trp Ile Phe Tyr Asp Thr Gly Tyr Thr Glu Arg Tyr Met
            195                 200                 205
Gly His Pro Asp Gln Asn Glu Gln Gly Tyr Tyr Leu Gly Ser Val Ala
            210                 215                 220
Met Gln Ala Glu Lys Phe Pro Ser Glu Pro Asn Arg Leu Leu Leu Leu
225                 230                 235                 240
His Gly Phe Leu Asp Glu Asn Val His Phe Ala His Thr Ser Ile Leu
                245                 250                 255
Leu Ser Phe Leu Val Arg Ala Gly Lys Pro Tyr Asp Leu Gln Ile Tyr
            260                 265                 270
Pro Gln Glu Arg His Ser Ile Arg Val Pro Glu Ser Gly Glu His Tyr
            275                 280                 285
Glu Leu His Leu Leu His Tyr Leu Gln Glu Asn Leu Gly Ser Arg Ile
            290                 295                 300
Ala Ala Leu Lys Val Ile
305                 310
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<210> 4
<211> 1197
<212> DNA
<213> Homo Sapiens

<400> 4
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agcactgtga cttctttata agtaagtata gtaaccagaa gaatccacac tgtgtgtccc 180
tttacaagct atcaagtcct gaagatgacc caacttgcaa aacaaaggaa ttttgggcca 240
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aaagtactac tggatttaca ttgtatggga tgctctacaa gcctcatgat ctacagcctg 360
gaaagaaata tcctactgtg ctgttcatat atggtggtcc tcagggtcaa atagaaattg 420
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gtgtgggcat ccacggctgg tcctatggag gatacctctc cctgatggca ttaatgcaga 540
ggtcagatat cttcagggtt gctattgctg gggccccagt cactctgtgg atcttctatg 600
atacaggata cacggaacgt tatatgggtc accctgacca gaatgaacag ggctattact 660
taggatctgt ggccatgcaa gcagaaaagt tcccctctga accaaatcgt ttactgctct 720
tacatggttt cctggatgag aatgtccatt ttgcacatac cagtatatta ctgagttttt 780
tagtgagggc tggaaagcca tatgatttac agatctatcc tcaggagaga cacagcataa 840
gagttcctga atcgggagaa cattatgaac tgcatctttt gcactacctt caagaaaacc 900
ttggatcacg tattgctgct ctaaaagtga tataattttg acctgtgtag aactctctgg 960
tatacactgg ctatttaacc aaatgaggag gtttaatcaa cagaaacac  agaattgatc 1020
atcacatttt gatacctgcc atgtaacatc tactcctgaa aataaatgtg gtgccatgca 1080
ggggtctacg gtttgtggta gtaatctaat accttaaccc cacatgctca aaatcaaatg 1140
atacatattc ctgagagacc cagcaatacc ataagaatta ctaaaaaaaa aaaaaaa    1197
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<210> 5
<211> 465
<212> PRT
<213> Homo Sapiens
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Ile Asp Ala Glu Gly Arg Ile Ile Asp Val Ile Asp Lys Glu Leu Ile
            20                  25                  30
Gln Pro Phe Glu Ile Leu Phe Glu Gly Val Glu Tyr Ile Ala Arg Ala
            35                  40                  45
Gly Trp Thr Pro Glu Gly Lys Tyr Ala Trp Ser Ile Leu Leu Asp Arg
    50                  55                  60
Ser Gln Thr Arg Leu Gln Ile Val Leu Ile Ser Pro Glu Leu Phe Ile
65                  70                  75                  80
Pro Val Glu Asp Asp Val Met Glu Arg Gln Arg Leu Ile Glu Ser Val
                85                  90                  95
Pro Asp Ser Val Thr Pro Leu Ile Ile Tyr Glu Glu Thr Thr Asp Ile
                100                 105                 110
Trp Ile Asn Ile His Asp Ile Phe His Val Phe Pro Gln Ser His Glu
            115                 120                 125
Glu Glu Ile Glu Phe Ile Phe Ala Ser Glu Cys Lys Thr Gly Phe Arg
    130                 135                 140
His Leu Tyr Lys Ile Thr Ser Ile Leu Lys Glu Ser Lys Tyr Lys Arg
145                 150                 155                 160
Ser Ser Gly Gly Leu Pro Ala Pro Ser Asp Phe Lys Cys Pro Ile Lys
                165                 170                 175
Glu Glu Ile Ala Ile Thr Ser Gly Glu Trp Glu Val Leu Gly Arg His
            180                 185                 190
Gly Ser Asn Ile Gln Val Asp Glu Val Arg Arg Leu Val Tyr Phe Glu
            195                 200                 205
Gly Thr Lys Asp Ser Pro Leu Glu His His Leu Tyr Val Val Ser Tyr
    210                 215                 220
Val Asn Pro Gly Glu Val Thr Arg Leu Thr Asp Arg Gly Tyr Ser His
225                 230                 235                 240
Ser Cys Cys Ile Ser Gln His Cys Asp Phe Phe Ile Ser Lys Tyr Ser
                245                 250                 255
Asn Gln Lys Asn Pro His Cys Val Ser Leu Tyr Lys Leu Ser Ser Pro
```

```
             260               265                 270
Glu Asp Asp Pro Thr Cys Lys Thr Lys Glu Phe Trp Ala Thr Ile Leu
             275               280                 285
Asp Ser Ala Gly Pro Leu Pro Asp Tyr Thr Pro Pro Glu Ile Phe Ser
         290               295                 300
Phe Glu Ser Thr Thr Gly Phe Thr Leu Tyr Gly Met Leu Tyr Lys Pro
305               310                 315                 320
His Asp Leu Gln Pro Gly Lys Lys Tyr Pro Thr Val Leu Phe Ile Tyr
                 325               330                 335
Gly Gly Pro Gln Val Ala Ile Ala Gly Ala Pro Val Thr Leu Trp Ile
             340               345                 350
Phe Tyr Asp Thr Gly Tyr Thr Glu Arg Tyr Met Gly His Pro Asp Gln
             355               360                 365
Asn Glu Gln Gly Tyr Tyr Leu Gly Ser Val Ala Met Gln Ala Glu Lys
         370               375                 380
Phe Pro Ser Glu Pro Asn Arg Leu Leu Leu Leu His Gly Phe Leu Asp
385               390                 395                 400
Glu Asn Val His Phe Ala His Thr Ser Ile Leu Leu Ser Phe Leu Val
                 405               410                 415
Arg Ala Gly Lys Pro Tyr Asp Leu Gln Ile Tyr Pro Gln Glu Arg His
             420               425                 430
Ser Ile Arg Val Pro Glu Ser Gly Glu His Tyr Glu Leu His Leu Leu
             435               440                 445
His Tyr Leu Gln Glu Asn Leu Gly Ser Arg Ile Ala Ala Leu Lys Val
     450               455                 460
Ile
465
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<210> 6
<211> 1669
<212> DNA
<213> Homo Sapiens

<400> 6

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aggagttgaa tatattgcca gagctggatg gactcctgag ggaaaatatg cttggtccat  180
cctactagat cgctcccaga ctcgcctaca gatagtgttg atctcacctg aattatttat  240
cccagtagaa gatgatgtta tggaaaggca gagactcatt gagtcagtgc ctgattctgt  300
gacgccacta attatctatg aagaaacaac agacatctgg ataaatatcc atgacatctt  360
tcatgttttt ccccaaagtc acgaagagga aattgagttt attttttgcct ctgaatgcaa  420
aacaggtttc cgtcatttat acaaaattac atctatttta aaggaaagca aatataaacg  480
atccagtggt gggctgcctg ctccaagtga tttcaagtgt cctatcaaag aggagatagc  540
aattaccagt ggtgaatggg aagttcttgg ccggcatgga tctaatatcc aagttgatga  600
agtcagaagg ctggtatatt ttgaaggcac caaagactcc ctttagagt atcaactgta  640
cgtagtcagt tacgtaaatc ctggagaggt gacaaggctg actgaccgtg ctactcaca  720
ttcttgctgc atcagtcagc actgtgactt cttttataagt aagtatagta accagaagaa  780
tccacactgt gtgtcccttt acaagctatc aagtcctgaa gatgacccaa cttgcaaaac  840
aaaggaattt tgggccacca ttttggattc agcaggtcct cttcctgact atactcctcc  900
agaaattttc tcttttgaaa gtactactgg atttacattg tatgggatgc tctacaagcc  960
tcatgatcta cagcctggaa agaaatatcc tactgtgctg ttcatatatg gtggtcctca 1020
ggttgctatt gctggggccc cagtcactct gtggatcttc tatgatacag gatacacgga 1080
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```
acgttatatg ggtcaccctg accagaatga acagggctat tacttaggat ctgtggccat 1140
gcaagcagaa aagttccccct ctgaaccaaa tcgtttactg ctcttacatg gtttcctgga 1200
tgagaatgtc cattttgcac ataccagtat attactgagt tttttagtga gggctggaaa 1260
gccatatgat ttacagatct atcctcagga gagacacagc ataagagttc ctgaatcggg 1320
agaacattat gaactgcatc ttttgcacta ccttcaagaa aaccttggat cacgtattgc 1380
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tgccatgtaa catctactcc tgaaataaa tgtggtgcca tgcaggggtc tacggtttgt 1560
ggtagtaatc taataccttta accccacatg ctcaaaatca aatgatacat attcctgaga 1620
gacccagcaa taccataaga attactaaaa aaaaaaaaaa aaaaaaaaa         1669
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<210> 7
<211> 360
<212> PRT
<213> Homo Sapiens

<400> 7
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Glu Glu Asp Ala Arg Ser Ala Gly Val Ala Thr Phe Val Leu Gln Glu
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Glu Phe Asp Arg Tyr Ser Gly Tyr Trp Trp Cys Pro Lys Ala Glu Thr
                20                  25                  30
Thr Pro Ser Gly Gly Lys Ile Leu Arg Ile Leu Tyr Glu Glu Asn Asp
             35                  40                  45
Glu Ser Glu Val Glu Ile Ile His Val Thr Ser Pro Met Leu Glu Thr
          50                  55                  60
Arg Arg Ala Asp Ser Phe Arg Tyr Pro Lys Thr Gly Thr Ala Asn Pro
65                  70                  75                  80
Lys Val Thr Phe Lys Met Ser Glu Ile Met Ile Asp Ala Glu Gly Arg
                85                  90                  95
Ile Ile Val Asp Glu Val Arg Arg Leu Val Tyr Phe Glu Gly Thr Lys
            100                 105                 110
Asp Ser Pro Leu Glu His His Leu Tyr Val Val Ser Tyr Val Asn Pro
         115                 120                 125
Gly Glu Val Thr Arg Leu Thr Asp Arg Gly Tyr Ser His Ser Cys Cys
      130                 135                 140
Ile Ser Gln His Cys Asp Phe Phe Ile Ser Lys Tyr Ser Asn Gln Lys
145                 150                 155                 160
Asn Pro His Cys Val Ser Leu Tyr Lys Leu Ser Ser Pro Glu Asp Asp
                165                 170                 175
Pro Thr Cys Lys Thr Lys Glu Phe Trp Ala Thr Ile Leu Asp Ser Ala
            180                 185                 190
Gly Pro Leu Pro Asp Tyr Thr Pro Pro Glu Ile Phe Ser Phe Glu Ser
         195                 200                 205
Thr Thr Gly Phe Thr Leu Tyr Gly Met Leu Tyr Lys Pro His Asp Leu
      210                 215                 220
Gln Pro Glu Lys Lys Tyr Pro Thr Val Leu Phe Ile Tyr Gly Gly Pro
225                 230                 235                 240
Gln Val Gln Leu Val Asn Asn Arg Phe Lys Gly Val Lys Tyr Phe Arg
                245                 250                 255
Leu Asn Thr Leu Ala Ser Leu Gly Tyr Val Val Val Val Ile Asp Asn
            260                 265                 270
Arg Gly Ser Cys His Arg Gly Leu Lys Phe Glu Gly Ala Phe Lys Tyr
         275                 280                 285
```

```
Lys Met Gly Gln Ile Glu Ile Asp Asp Gln Val Glu Gly Leu Gln Tyr
    290                 295             300
Leu Ala Ser Arg Tyr Asp Phe Ile Asp Leu Asp Arg Val Gly Ile His
305                 310             315                 320
Gly Trp Ser Tyr Gly Gly Tyr Leu Ser Leu Met Ala Leu Met Gln Arg
                325             330                 335
Ser Asp Ile Phe Arg Val Ala Ile Ala Gly Ala Pro Val Thr Leu Trp
                340             345                 350
Ile Phe Tyr Asp Thr Gly Tyr Thr
                355             360
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<210> 8
<211> 1083
<212> DNA
<213> Homo Sapiens

<400> 8
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tagaattcta tatgaagaaa atgatgaatc tgaggtggaa attattcatg ttacatcccc 180
tatgttggaa acaaggaggg cagattcatt ccgttatcct aaaacaggta cagcaaatcc 240
taaagtcact tttaagatgt cagaaataat gattgatgct gaaggaagga tcatagttga 300
tgaagtcaga aggctggtat attttgaagg caccaaagac tcccctttag agcatcacct 360
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